



99/786880
Rec'd PCT/PTO 15 FEB 2002

#10

SEQUENCE LISTING

ENTIS PHARMA S.A.

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> 16655

<140> PCT/EP99/07378

<141> 1999-09-13

<150> EP98402255.8

<151> 1998-09-11

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 1

attcatccca tcagtgcaga aagtttgc at gccatttac aacaattaat aaatgataaa 60
cctcaagaga cagtacaaga atcgtctgat ttattacaat ttatcccagt ctctagatta 120
cctgtcaaag ataatat tttt gaaatttgat caaattaatc ataaatctcc tacttttgatt 180
atgggtatat tgaatatgac tcctgattca tttagtgatg gtgggaaaca ttttgaaaaa 240
gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300
gacattggag gagtttccac acgaccagga agtggtgaac cactgagga agaagaattg 360
gaacgtgtga ttccattaat tagagctatt cgtcaatca 399

<210> 2

<211> 2367

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(2364)

<220>

<221> gene

<222> (1)..(2364)

<223> gene CaNL256

<400> 2

atg ttg aaa aac gat acc gtt ttc act aaa gat att tct tgt acg gcg	48
Met Leu Lys Asn Asp Thr Val Phe Thr Lys Asp Ile Ser Cys Thr Ala	
1 5 10 15	
ata act ggt aaa gat gcc tgg aat cgg cca aca cca caa cca atc act	96
Ile Thr Gly Lys Asp Ala Trp Asn Arg Pro Thr Pro Gln Pro Ile Thr	
20 25 30	
ata tca tta tct ttc aat act gat ttc cat aag gca tcg gaa ttg gat	144
Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp	
35 40 45	
aat ttg aaa tac tca att aat tat gct gtt att acc aga aat gta act	192
Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr	
50 55 60	
gaa ttt atg aaa tca aat gag cat tta aat ttc aag tca tta gga aat	240
Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn	
65 70 75 80	
att gct caa gca att agt gat att gga tta gat caa tct aga ggt ggt	288
Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly	
85 90 95	
gga tct att gtg gat gtg acg ata aaa agt ttg aaa tca gaa ata aga	336
Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg	
100 105 110	
gct gaa agt gtc gaa tat aaa att aat aga aac act ttg ggt caa ccc	384
Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro	
115 120 125	
gtt cca tta gat att ttc caa gtt aat aaa ttg aga tta ttg acg att	432
Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile	
130 135 140	
att gga gtt ttc aca ttt gaa aga tta caa aaa caa ata gtt gat gtt	480
Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val	
145 150 155 160	
gat ttg caa ttt aaa att gaa cct aat tcc aat tta tat ttc cat caa	528
Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln	
165 170 175	
ata att gct gat att gtt tca tac gtg gaa tca tct aat ttc aaa act	576
Ile Ile Ala Asp Ile Val Ser Tyr Val Glu Ser Ser Asn Phe Lys Thr	
180 185 190	
gta gaa gca ttg gtg tct aag att ggt caa ttg aca ttt cag aaa tat	624
Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr	
195 200 205	
gac gga gta gct gaa gtt gtt gct act gtc act aaa ccg aat gca ttt	672-
Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe	
210 215 220	

agt cat gtt gaa ggt gtt gga gta tca tct acc atg gtc aaa gac aat	720
Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn	
225 230 235 240	
ttc aaa gat atg gaa cca gtt aaa ttt gaa aac aca att gct caa act	768
Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr	
245 250 255	
aat aga gca ttc aat tta cct gtt gaa aat gag aaa act gag gat tat	816
Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr	
260 265 270	
acc ggg tac cac act gca ttt att gcc ttt gga tcc aat act gga aat	864
Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn	
275 280 285	
caa gta gaa aat att acc aat tca ttc gaa ttg ttg caa aaa tat gga	912
Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly	
290 295 300	
atc acc ata gaa gca act tca tca ttg tac att tct aaa cca atg tat	960
Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr	
305 310 315 320	
tac ttg gat caa cca gat ttt ttc aat gga gta att aaa gtg aat ttc	1008
Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325 330 335	
caa aac att tca cct ttc cag ttg ttg aaa att cta aaa gat att gaa	1056
Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu	
340 345 350	
tat aaa cat tta gaa agg aaa aaa gac ttt gat aat ggg ccc aga tca	1104
Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser	
355 360 365	
ata gat ttg gat att ata cta tat gac gat tta caa tta aat acc gag	1152
Ile Asp Leu Asp Ile Ile Leu Tyr Asp Asp Leu Gln Leu Asn Thr Glu	
370 375 380	
aat cta att att cca cat aaa tca atg tta gaa aga aca ttt gta tta	1200
Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu	
385 390 395 400	
caa cca tta tgt gaa gta ttg ccc cct gat tat att cat ccc atc agt	1248
Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
405 410 415	
gca gaa agt ttg cat agc cat tta caa caa tta ata aat gat aaa cct	1296
Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro	
420 425 430	
caa gag aca gta caa gaa tcg tct gat tta tta caa ttt atc cca gtc	1344
Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val	-
435 440 445	
tct aga ttg cct gtc aaa gat aat att ttg aaa ttt gat caa att aat	1392

Ser	Arg	Leu	Pro	Val	Lys	Asp	Asn	Ile	Leu	Lys	Phe	Asp	Gln	Ile	Asn		
450						455					460						
cat	aaa	tct	cct	act	ttg	att	atg	ggg	ata	ttg	aat	atg	act	cct	gat	1440	
His	Lys	Ser	Pro	Thr	Leu	Ile	Met	Gly	Ile	Leu	Asn	Met	Thr	Pro	Asp		
465					470					475					480		
tca	ttt	agt	gat	ggg	aaa	cat	ttt	gga	aaa	gaa	cta	gat	aat	act		1488	
Ser	Phe	Ser	Asp	Gly	Gly	Lys	His	Phe	Gly	Lys	Glu	Leu	Asp	Asn	Thr		
				485					490					495			
gtg	aag	cag	gca	gag	aaa	tta	gtc	agt	gag	ggg	gct	acg	att	att	gac	1536	
Val	Lys	Gln	Ala	Glu	Lys	Leu	Val	Ser	Glu	Gly	Ala	Thr	Ile	Ile	Asp		
			500					505						510			
att	gga	gga	gtt	tcc	aca	cgc	cca	gga	agt	gtt	gaa	ccc	act	gag	gaa	1584	
Ile	Gly	Gly	Val	Ser	Thr	Arg	Pro	Gly	Ser	Val	Glu	Pro	Thr	Glu	Glu		
			515				520							525			
gaa	gaa	ttg	gaa	cgt	gtg	att	cca	tta	att	aaa	gct	att	cgt	caa	tca	1632	
Glu	Glu	Leu	Glu	Arg	Val	Ile	Pro	Leu	Ile	Lys	Ala	Ile	Arg	Gln	Ser		
			530			535					540						
ctg	aac	cct	gat	tta	ctg	aag	gtg	ttg	att	tcg	gtt	gat	act	tat	cgt	1680	
Leu	Asn	Pro	Asp	Leu	Leu	Lys	Val	Leu	Ile	Ser	Val	Asp	Thr	Tyr	Arg		
545					550					555					560		
agg	aac	gtt	gct	gaa	caa	agt	tta	ctt	gtg	ggg	gct	gac	ata	atc	aac	1728	
Arg	Asn	Val	Ala	Glu	Gln	Ser	Leu	Leu	Val	Gly	Ala	Asp	Ile	Ile	Asn		
				565					570					575			
gat	atc	tca	atg	ggc	aaa	tat	gat	gaa	aaa	ata	ttt	gat	gtg	gtt	gct	1776	
Asp	Ile	Ser	Met	Gly	Lys	Tyr	Asp	Glu	Lys	Ile	Phe	Asp	Val	Val	Ala		
			580					585						590			
aaa	tac	gga	tgt	cct	tat	atc	atg	aat	cat	act	cga	gga	tca	cct	aaa	1824	
Lys	Tyr	Gly	Cys	Pro	Tyr	Ile	Met	Asn	His	Thr	Arg	Gly	Ser	Pro	Lys		
			595				600							605			
acc	atg	tct	aaa	ttg	acc	aat	tat	gaa	tca	aat	aca	aat	gat	gat	att	1872	
Thr	Met	Ser	Lys	Leu	Thr	Asn	Tyr	Glu	Ser	Asn	Thr	Asn	Asp	Asp	Ile		
			610				615					620					
atc	gaa	tat	ata	att	gat	cct	aaa	tta	gga	cat	caa	gaa	ttg	gat	ttg	1920	
Ile	Glu	Tyr	Ile	Ile	Asp	Pro	Lys	Leu	Gly	His	Gln	Glu	Leu	Asp	Leu		
625					630					635					640		
tca	cct	gaa	atc	aag	aat	tta	ctc	aat	gga	atc	agt	cgt	gaa	ttg	agt	1968	
Ser	Pro	Glu	Ile	Lys	Asn	Leu	Leu	Asn	Gly	Ile	Ser	Arg	Glu	Leu	Ser		
				645					650					655			
tta	caa	atg	ttt	aaa	gcc	atg	gct	aaa	gga	gtg	aaa	aaa	tgg	caa	att	2016	
Leu	Gln	Met	Phe	Lys	Ala	Met	Ala	Lys	Gly	Val	Lys	Lys	Trp	Gln	Ile		
			660					665						670			
att	ttg	gat	cct	ggg	att	gga	ttt	gct	aaa	aat	ttg	aat	caa	aat	tta	2064	
Ile	Leu	Asp	Pro	Gly	Ile	Gly	Phe	Ala	Lys	Asn	Leu	Asn	Gln	Asn	Leu		

675

680

685

gca gtt att cgt aat gcc tcg ttt ttt aaa aaa tat tct att caa att 2112
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile
 690 695 700

aat gaa cgt gtt gat gat gtg aca atc aaa cat aaa tat tta agt ttt 2160
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
 705 710 715 720

aat ggt gct tgt gtt ttg gtg ggg aca tca aga aag aag ttt ttg ggg 2208
 Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
 725 730 735

aca tta act ggt aat gaa gtg cct ctg gat cga gta ttt ggc act ggt 2256
 Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
 740 745 750

gca aca gtg tct gcg tgt att gaa caa aac act gat att gta aga gtt 2304
 Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
 755 760 765

cat gat gtt aaa gaa atg aaa gat gta gta tgt ata agt gat gca att 2352
 His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile
 770 775 780

tat aaa aat gta taa 2367
 Tyr Lys Asn Val
 785

<210> 3

<211> 788

<212> PRT

<213> Candida albicans

<400> 3

Met Leu Lys Asn Asp Thr Val Phe Thr Lys Asp Ile Ser Cys Thr Ala
 1 5 10 15

Ile Thr Gly Lys Asp Ala Trp Asn Arg Pro Thr Pro Gln Pro Ile Thr
 20 25 30

Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp
 35 40 45

Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr
 50 55 60

Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn
 65 70 75 80

Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly
 85 90 95

Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg
 100 105 110

Ala	Glu	Ser	Val	Glu	Tyr	Lys	Ile	Asn	Arg	Asn	Thr	Leu	Gly	Gln	Pro	115	120	125
Val	Pro	Leu	Asp	Ile	Phe	Gln	Val	Asn	Lys	Leu	Arg	Leu	Leu	Thr	Ile	130	135	140
Ile	Gly	Val	Phe	Thr	Phe	Glu	Arg	Leu	Gln	Lys	Gln	Ile	Val	Asp	Val	145	150	155
Asp	Leu	Gln	Phe	Lys	Ile	Glu	Pro	Asn	Ser	Asn	Leu	Tyr	Phe	His	Gln	165	170	175
Ile	Ile	Ala	Asp	Ile	Val	Ser	Tyr	Val	Glu	Ser	Ser	Asn	Phe	Lys	Thr	180	185	190
Val	Glu	Ala	Leu	Val	Ser	Lys	Ile	Gly	Gln	Leu	Thr	Phe	Gln	Lys	Tyr	195	200	205
Asp	Gly	Val	Ala	Glu	Val	Val	Ala	Thr	Val	Thr	Lys	Pro	Asn	Ala	Phe	210	215	220
Ser	His	Val	Glu	Gly	Val	Gly	Val	Ser	Ser	Thr	Met	Val	Lys	Asp	Asn	225	230	235
Phe	Lys	Asp	Met	Glu	Pro	Val	Lys	Phe	Glu	Asn	Thr	Ile	Ala	Gln	Thr	245	250	255
Asn	Arg	Ala	Phe	Asn	Leu	Pro	Val	Glu	Asn	Glu	Lys	Thr	Glu	Asp	Tyr	260	265	270
Thr	Gly	Tyr	His	Thr	Ala	Phe	Ile	Ala	Phe	Gly	Ser	Asn	Thr	Gly	Asn	275	280	285
Gln	Val	Glu	Asn	Ile	Thr	Asn	Ser	Phe	Glu	Leu	Leu	Gln	Lys	Tyr	Gly	290	295	300
Ile	Thr	Ile	Glu	Ala	Thr	Ser	Ser	Leu	Tyr	Ile	Ser	Lys	Pro	Met	Tyr	305	310	315
Tyr	Leu	Asp	Gln	Pro	Asp	Phe	Phe	Asn	Gly	Val	Ile	Lys	Val	Asn	Phe	325	330	335
Gln	Asn	Ile	Ser	Pro	Phe	Gln	Leu	Leu	Lys	Ile	Leu	Lys	Asp	Ile	Glu	340	345	350
Tyr	Lys	His	Leu	Glu	Arg	Lys	Lys	Asp	Phe	Asp	Asn	Gly	Pro	Arg	Ser	355	360	365
Ile	Asp	Leu	Asp	Ile	Ile	Leu	Tyr	Asp	Asp	Leu	Gln	Leu	Asn	Thr	Glu	370	375	380
Asn	Leu	Ile	Ile	Pro	His	Lys	Ser	Met	Leu	Glu	Arg	Thr	Phe	Val	Leu	385	390	395
Gln	Pro	Leu	Cys	Glu	Val	Leu	Pro	Pro	Asp	Tyr	Ile	His	Pro	Ile	Ser	405	410	415

Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro
 420 425 430
 Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val
 435 440 445
 Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn
 450 455 460
 His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp
 465 470 475 480
 Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr
 485 490 495
 Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp
 500 505 510
 Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu
 515 520 525
 Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Lys Ala Ile Arg Gln Ser
 530 535 540
 Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg
 545 550 555 560
 Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn
 565 570 575
 Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala
 580 585 590
 Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys
 595 600 605
 Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile
 610 615 620
 Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu
 625 630 635 640
 Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser
 645 650 655
 Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile
 660 665 670
 Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu
 675 680 685
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile
 690 695 700
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
 705 710 715 720

Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
725 730 735

Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
740 745 750

Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
755 760 765

His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile
770 775 780

Tyr Lys Asn Val
785

<210> 4

<211> 647

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 4

agatttcaat tgggtattcc cagtaataaa aagaaagatc gatcatcaat tatggtgctt 60
aaaaaaatgt gggattctca attacaatca ttatttaaac atgttgacgg tgcataaaaa 120
tttgtgcaac cattacccaa tagacacatt gtcgcggaaa gtggacgatg gtttgaagtt 180
aatgtgggga attggaaacc aagttatcca actcatttat ttatatttaa tgatttaatt 240
ttaattgccg ttaaaaaatc atcatctagt agtcaggaac ctactacagg gggaagtaat 300
ggtggttcaa aatcgagatt acaagcgggt caatgttggc ccttaactca agtatcatta 360
caacaaatca aatcaccgaa aaaagatgac gataagatgt attttatcaa tcttaaatcc 420
aaatctttta gttatgtata cctgacggat cgttatgatc attttgtgaa agttacggaa 480
gcatttaata aaggtagaaa tgaaatgatt caaagtgaag gattattaga ttcaagactt 540
tcattctcctt caaataataa tggagattct aaagaagaga aacgacaatt acgggaatca 600
ttaagaaact caggcaatta taaagaagga gttactgatg atgccgg 647

<210> 5

<211> 2373

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(2373)

<220>

<221> gene

<222> (1)..(2373)

<223> gene CaBR102

<400> 5

atg gat aat ctt gat ccc aat tct agt tta caa gta gag aaa tta cga	48
Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg	
1 5 10 15	
aac agg aaa agc agg gct gta tgg cag aat aac aac act tct act cat	96
Asn Arg Lys Ser Arg Ala-Val Trp Gln Asn Asn Asn Thr Ser Thr His	
20 25 30	
aat aat cct tat gct aat tta agc act ggt gaa aaa agt agg agt cgc	144
Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg	
35 40 45	
cat aac act ggt agt tct tat gtt tct cca tat ggc ggc ggt aat gga	192
His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly	
50 55 60	
gag gag aat gct tat act ggg aat aac aac aaa tca aat act agt ggt	240
Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly	
65 70 75 80	
aat tta tta caa gtt cct gga gca gga gga gga gga gat ttg aat tct	288
Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser	
85 90 95	
aat aag aaa caa agt cga aga atg agt att cat gta tca gct cgt caa	336
Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln	
100 105 110	
cat gga aga tca ttt tca caa act ggt cca att gat atg gca aat tta	384
His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu	
115 120 125	
ccg gca tta cct aaa ata ggt ggt gtt act act agt ggt gtt ggc ggt	432
Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly	
130 135 140	
gct ggt ggt gat gtt atg aca agg act ggg gga ttg acg ata gaa caa	480
Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln	
145 150 155 160	
aaa ata ttc aaa gaa tta agt caa gga tca gca gct gaa gtt gat gat	528
Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp	
165 170 175	
tat tac aag aca tta ttg aaa cag aaa aat tta atc act cgt gac att	576
Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile	
180 185 190	
aag gat aat att aat cag aat caa aaa aat att tta caa tta aca aaa	624
Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys	

195	200	205	
gac ttg aaa gag acc caa gaa gaa ttg att gaa ttg aga gga acc act Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr 210 215 220			672
aaa gaa tta tat gaa gtt tta ggt tat ttc aaa gaa tca gct caa cgt Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg 225 230 235 240			720
aga tta gaa ttg gaa ttt gaa cca gaa aca caa aaa gaa ctt cat ctg Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu 245 250 255			768
cct caa aaa agt aat caa ttg ggt att cct agt aat aaa aag aaa gat Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp 260 265 270			816
cga tca tca att atg gtg ctt aaa aaa atg tgg gat tct caa tta caa Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln 275 280 285			864
tca tta ttt aaa cat gtt gac ggt gca tca aaa ttt gtc caa cca tta Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu 290 295 300			912
ccc aat aga cac att gtc gcg gaa agt gga cga tgg ttt gaa gtt aat Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn 305 310 315 320			960
gtg ggg aat tgg aaa cca agt tat cca act cat tta ttt ata ttt aat Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn 325 330 335			1008
gat tta att tta att act gtt aaa aaa tca tca tct agt agt cag gaa Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu 340 345 350			1056
cct act aca ggg gga agt aat ggt ggt tca aaa tcg aga tta caa gcg Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala 355 360 365			1104
gtt caa tgt tgg ccc tta act caa gta tca tta caa caa atc aaa tca Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser 370 375 380			1152
ccg aaa aaa gat gac gat aag atg tat ttt atc aat ctt aaa tcc aaa Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys 385 390 395 400			1200
tct tta agt tat gta tac ctg acg gat cgt tat gat cat ttt gtg aaa Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys 405 410 415			1248
gtt acg gaa gca ttt aat aaa ggt aga aat gaa atg att caa agt gaa Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu 420 425 430			1296

aga tta tta gat tca aga ctt tca tct cct tca aat aat aat gga gat	1344
Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp	
435 440 445	
tct aaa gaa gag aaa cga caa tta cgg gaa tca tta aga aac tca ggc	1392
Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly	
450 455 460	
aat tat aaa gaa gga gtt act gat gat gcc ggt gga gct gca act ggt	1440
Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly	
465 470 475 480	
ggt ggt agg aaa agt gcc ggt act cct aat aga aat agt act gat tac	1488
Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr	
485 490 495	
gtt tta cat gat ata tct gct cga gta cat tca cgt aat cga tca caa	1536
Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln	
500 505 510	
gat tta ggg aat aat ttc aaa tta gct aat aat ggg aaa tca caa ttt	1584
Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe	
515 520 525	
ttc aat gaa atc aaa act tta gaa gat cga tta gat gat gtt gac gtt	1632
Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val	
530 535 540	
gaa ata tcg cat aat caa tat gct gaa gcc gtg gaa tta ata tca ata	1680
Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile	
545 550 555 560	
att gaa tct aaa tta cgt aat att gaa aat gca tta act aat caa cgt	1728
Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg	
565 570 575	
aat gga ggt aaa aat gtc aat att gct gat gaa tta tta ctt tta gat	1776
Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp	
580 585 590	
gta tca aaa ttg aaa att aaa aat cgg aaa gaa aat gta tct aat gga	1824
Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly	
595 600 605	
tta ata ttt gat tta caa cat aat ata gct aaa ctt aaa caa gat gat	1872
Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp	
610 615 620	
att gat aat att ttg acg tta ttt gat aat tta gag caa tta gat cga	1920
Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg	
625 630 635 640	
ggg gtt caa gga tat ttg gat tca atg tca gct tat tta tca act aca	1968
Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr	
645 650 655	

gta tca aaa tta att gtt ggt tta caa gga tca acg aaa atc gat gtt 2016
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

gtt aat tat ctt tcc aat tta atg gtt att aat gta tcg att gtg aaa 2064
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt 2112
 Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa 2160
 His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg 2208
 Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa 2256
 Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

gtt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca 2304
 Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt 2352
 Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

gag tct ata tta aat ctt gaa 2373
 Glu Ser Ile Leu Asn Leu Glu
 785 790

<210> 6

<211> 791

<212> PRT

<213> Candida albicans

<400> 6

Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg
 1 5 10 15

Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His
 20 25 30

Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg
 35 40 45

His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly
 50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly
 65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser
 85 90 95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln
 100 105 110

His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu
 115 120 125

Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly
 130 135- 140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln
 145 150 155 160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp
 165 170 175

Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile
 180 185 190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys
 195 200 205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr
 210 215 220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg
 225 230 235 240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu
 245 250 255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp
 260 265 270

Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln
 275 280 285

Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu
 290 295 300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn
 305 310 315 320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn
 325 330 335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu
 340 345 350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala
 355 360 365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser
 370 375 380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys
 385 390 395 400
 Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys
 405 410 415
 Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu
 420 425 430
 Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp
 435 440 445
 Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly
 450 455 460
 Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly
 465 470 475 480
 Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr
 485 490 495
 Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln
 500 505 510
 Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe
 515 520 525
 Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val
 530 535 540
 Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile
 545 550 555 560
 Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg
 565 570 575
 Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp
 580 585 590
 Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly
 595 600 605
 Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp
 610 615 620
 Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg
 625 630 635 640
 Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
770 775 780

Glu Ser Ile Leu Asn Leu Glu
785 790

<210> 7

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 7

ctgcagtaaa cctccagat ataacagact ctttatgtcc agtgatttcg ccaacaaatc 60
ttggtggttg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120
ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180
aagtccatga attgttgac atgtcaattt ctaaagtctc atgctcatca tctaattcca 240
tctctcctc tcttctcatcg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300
cattaacatt gatataattct tcttgagtat cgtctacgac gtc 343

<210> 8

<211> 1248

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1245)

<220>

<221> gene

<222> (1)..(1245)

<223> gene CaIR012

<400> 8

atg tca cac caa caa gaa gac gtc gta gac gat act caa gaa gaa tat	48
Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr	
1 5 10 15	
atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala	
20 25 30	
cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	
act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
50 55 60	
cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met	
65 70 75 80	
gta ttg act ggg ggt ggt gac aac acg gca tac tta tgg acc aca cac	288
Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His	
85 90 95	
acc caa cca cca aga ttt gtt ggc gaa atc act gga cat aaa gag tct	336
Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser	
100 105 110	
gtt ata tct gga ggg ttt act gca gac ggc aag ttt gtt gtt act gca	384
Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala	
115 120 125	
gac atg aat gga tta att caa gtt ttc aaa gcc aca aaa gga ggt gaa	432
Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu	
130 135 140	
cag tgg gtg aaa ttt ggt gaa ttg gac gaa gtt gaa gaa gtg ttg ttt	480
Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe	
145 150 155 160	
gtt act gtg cat cca aca tta cca ttc ttt gcc ttt ggt gct acc gat	528
Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp	
165 170 175	
gga tct ata tgg gtc tac caa ata gac gaa tcc agt aaa ctg cta gtg	576
Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val	
180 185 190	
caa att atg tct ggg ttc tca cac aca tta gaa tgt aat ggt gct gta	624
Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val	
195 200 205	
ttt ata caa gga aaa gat gaa aat gat ttg aca ttg gtc tct ata agt	672
Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser	

210	215	220	
gaa gat ggt act gtg	gtg aac tgg aac tgt ttt	aca gga caa gtg aat	720
Glu Asp Gly Thr Val	Val Asn Trp Asn Cys Phe	Thr Gly Gln Val Asn	
225	230	235 240	
tat aaa ttg caa cct cat	gat gac ttt aaa gga gtt	gaa agt ccg tgg	768
Tyr Lys Leu Gln Pro	His Asp Asp Phe Lys	Gly Val Glu Ser Pro Trp	
	245	250 255	
gtc acg gtc aaa gta cat	ggt aat ctt gtg gcc att	ggt ggc aga gat	816
Val Thr Val Lys Val	His Gly Asn Leu Val	Ala Ile Gly Gly Arg Asp	
	260	265 270	
ggc cag cta tca att gtg	aac aat gac act ggt	aaa atc gtt cat act	864
Gly Gln Leu Ser Ile	Val Asn Asn Asp Thr	Gly Lys Ile Val His Thr	
	275	280 285	
ctt aaa aca ttg gat aat	gtc gac gac att gca	gaa ctc tca att gag	912
Leu Lys Thr Leu Asp	Asn Val Asp Asp Ile	Ala Glu Leu Ser Ile Glu	
	290 295	300	
gca ttg agt tgg tgt gaa	agc aaa aat att aac	ctc ttg gca gtg ggt	960
Ala Leu Ser Trp Cys	Glu Ser Lys Asn Ile	Asn Leu Leu Ala Val Gly	
305	310 315	320	
ttg gtt tct ggt gac gtt	tta tta ttt gat act	cag caa tgg aga ttg	1008
Leu Val Ser Gly Asp	Val Leu Leu Phe Asp	Thr Gln Gln Trp Arg Leu	
	325	330 335	
aga aag aac ttg aaa gtt	gac gat gcc atc acc	aaa tta caa ttt gtt	1056
Arg Lys Asn Leu Lys	Val Asp Asp Ala Ile	Thr Lys Leu Gln Phe Val	
	340	345 350	
ggc gaa acc ccc att ttg	gtg gga agt agt atg	gat ggt aaa att tac	1104
Gly Glu Thr Pro Ile	Leu Val Gly Ser Ser	Met Asp Gly Lys Ile Tyr	
	355	360 365	
aaa tgg gac gct aga act	ggt gaa gag ttg ttt	gct ggt gtg gga cac	1152
Lys Trp Asp Ala Arg	Thr Gly Glu Glu Leu	Phe Ala Gly Val Gly His	
	370 375	380	
aac atg gga gta ttg gac	ttt gct att tta gat	gga ggt aaa aag ttg	1200
Asn Met Gly Val Leu	Asp Phe Ala Ile Leu	Asp Gly Gly Lys Lys Leu	
385	390 395	400	
gtt act gct ggt gat gaa	ggt gtt tca ttg gtc	ttt gta cat gaa tag	1248
Val Thr Ala Gly Asp	Glu Gly Val Ser Leu	Val Phe Val His Glu	
	405	410 415	

<210> 9

<211> 415

<212> PRT

<213> Candida albicans

<400> 9

Met	Ser	His	Gln	Gln	Glu	Asp	Val	Val	Asp	Asp	Thr	Gln	Glu	Glu	Tyr	1	5	10	15
Ile	Asn	Val	Asn	Glu	Val	Ala	Glu	Glu	Val	Ala	Asp	Asp	Asp	Gln	Ala	20	25	30	
Pro	Pro	Asp	Glu	Glu	Asp	Glu	Glu	Met	Glu	Leu	Asp	Asp	Glu	His	Glu	35	40	45	
Thr	Leu	Glu	Ile	Asp	Met	Ser	Asn	Asn	Ser	Trp	Thr	Tyr	Phe	Asp	Lys	50	55	60	
His	Thr	Asp	Ser	Ile	Phe	Thr	Ile	Phe	Ser	His	Pro	Lys	Leu	Pro	Met	65	70	75	80
Val	Leu	Thr	Gly	Gly	Gly	Asp	Asn	Thr	Ala	Tyr	Leu	Trp	Thr	Thr	His	85	90	95	
Thr	Gln	Pro	Pro	Arg	Phe	Val	Gly	Glu	Ile	Thr	Gly	His	Lys	Glu	Ser	100	105	110	
Val	Ile	Ser	Gly	Gly	Phe	Thr	Ala	Asp	Gly	Lys	Phe	Val	Val	Thr	Ala	115	120	125	
Asp	Met	Asn	Gly	Leu	Ile	Gln	Val	Phe	Lys	Ala	Thr	Lys	Gly	Gly	Glu	130	135	140	
Gln	Trp	Val	Lys	Phe	Gly	Glu	Leu	Asp	Glu	Val	Glu	Glu	Val	Leu	Phe	145	150	155	160
Val	Thr	Val	His	Pro	Thr	Leu	Pro	Phe	Phe	Ala	Phe	Gly	Ala	Thr	Asp	165	170	175	
Gly	Ser	Ile	Trp	Val	Tyr	Gln	Ile	Asp	Glu	Ser	Ser	Lys	Leu	Leu	Val	180	185	190	
Gln	Ile	Met	Ser	Gly	Phe	Ser	His	Thr	Leu	Glu	Cys	Asn	Gly	Ala	Val	195	200	205	
Phe	Ile	Gln	Gly	Lys	Asp	Glu	Asn	Asp	Leu	Thr	Leu	Val	Ser	Ile	Ser	210	215	220	
Glu	Asp	Gly	Thr	Val	Val	Asn	Trp	Asn	Cys	Phe	Thr	Gly	Gln	Val	Asn	225	230	235	240
Tyr	Lys	Leu	Gln	Pro	His	Asp	Asp	Phe	Lys	Gly	Val	Glu	Ser	Pro	Trp	245	250	255	
Val	Thr	Val	Lys	Val	His	Gly	Asn	Leu	Val	Ala	Ile	Gly	Gly	Arg	Asp	260	265	270	
Gly	Gln	Leu	Ser	Ile	Val	Asn	Asn	Asp	Thr	Gly	Lys	Ile	Val	His	Thr	275	280	285	
Leu	Lys	Thr	Leu	Asp	Asn	Val	Asp	Asp	Ile	Ala	Glu	Leu	Ser	Ile	Glu	290	295	300	

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
305 310 315 320

Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
355 360 365

Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
370 375 380

Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu
385 390 395 400

Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu
405 410 415

<210> 10

<211> 5544

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(5541)

<220>

<221> gene

<222> (1)..(5541)

<223> gene CaJL039

<400> 10

atg agt ggc ata ttt aat tgg tcg ctg gat gtg ttt gcc gat att tat 48
Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr
1 5 10 15

aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc 96
Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
20 25 30

acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct 144
Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
35 40 45

ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg 192
Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
50 55 60

ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att 240
Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
65 70 75 80

act gga gtt tta tca aat gaa ttg gat tta gat gaa cta aat aca gca	288
Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala	
85 90 95	
gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc	336
Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser	
100 105 110	
att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata	384
Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile	
115 120 125	
cta aac att gtt gga tac tta gtt tgc cat aaa cgt tta gat atc atc	432
Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile	
130 135 140	
act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc	480
Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser	
145 150 155 160	
aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa	528
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln	
165 170 175	
aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat	576
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn	
180 185 190	
tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt	624
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val	
195 200 205	
gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac	672
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn	
210 215 220	
aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa	720
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu	
225 230 235 240	
gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag	768
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys	
245 250 255	
aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag	816
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys	
260 265 270	
act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc	864
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser	
275 280 285	
aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa	912
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu	
290 295 300	
ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag	960

Ile Val Thr Ser Phe	Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys	
305	310	315 320
cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta		1008
Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu		
	325 330 335	
aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta		1056
Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu		
	340 345 350	
tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac		1104
Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp		
	355 360 365	
tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca		1152
Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro		
	370 375 380	
cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg		1200
Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu		
	385 390 395 400	
aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att		1248
Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile		
	405 410 415	
tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct		1296
Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro		
	420 425 430	
ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt		1344
Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val		
	435 440 445	
atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg		1392
Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu		
	450 455 460	
aat gaa agt gac gaa gag gaa gaa gaa gaa gaa agc gac agc gac gaa		1440
Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu		
	465 470 475 480	
gat tct tcg acc cca aaa aac aaa gaa aaa tca gct ggg tta gac ctt		1488
Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu		
	485 490 495	
gac aag att gcc cag cgt gct gaa tta gaa agg ttc tac ttg gct ttc		1536
Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe		
	500 505 510	
gcg tac acc tac aac aat cga cct gaa ttg tgt gcg tta ttt tgg ggg		1584
Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly		
	515 520 525	
aac gag cag gta act cat gac att ata gga ttt att tcc tgg gga ctt		1632
Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu		

530	535	540	
gct aat aat acg tct ccg ttg atc act gca aca ttc tgc tta cta tta			1680
Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu			
545	550	555	560
ggg tcg ttg gca tct gct ggt gca gag gca act tca agg ata tgg gag			1728
Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu			
	565	570	575
att ctt gta cac aac aat aac aac gca agt acg aga aaa aat gat ttt			1776
Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe			
	580	585	590
tca aag gta tcc gtt gac tcc ctt tat gat tcg ttg aaa tat tac att			1824
Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile			
	595	600	605
gac tct tta aat gaa agc ttt gaa caa gat tta aat gcc caa ttg atg			1872
Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met			
	610	615	620
ttg aat cag aag aaa caa gat ttt ctc ttc agc acc aca aca agc aaa			1920
Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys			
	625	630	635
cag gac ctt gat gat tct ggc gag aat aga att gtt ata gag ttg gcc			1968
Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala			
	645	650	655
gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca			2016
Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala			
	660	665	670
att gtg aag aat ttg aac act aag aat gaa aga agc aaa gaa atc aaa			2064
Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys			
	675	680	685
tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa			2112
Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys			
	690	695	700
ttc gat aat ttg atc aat ggt agc agg ttc ctt caa gtt gat gct agc			2160
Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser			
	705	710	715
att caa agc aca aac aac ccc aaa ttt att gat ttg cca aat gtt ttc			2208
Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe			
	725	730	735
gtc agt gat gac tcg aga att ata ttg acg aac ctc att cta acc ttt			2256
Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe			
	740	745	750
tta ggc gat ttt gtt acc aac gat agt gat ccg tat att aga tat gag			2304
Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu			
	755	760	765

att tgg cgt tta gtc gat cga tgg atg tac cag ggg ttg cat agt ttg Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu 770 775 780	2352
cca gaa gac aag aaa gat gat gct ttt aga cat att aag aga aag tat Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr 785 790 795 800	2400
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu 805 810 815	2448
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu 820 825 830	2496
tta acc cca tat gca gat agt aat gaa gca ttc acc aag tac tcg ttg Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu 835 840 845	2544
ttg tat cct tgt gac tta gga tta ggg tat aga ttc aac aac caa ctt Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu 850 855 860	2592
gga att tgg cca tac att gaa ttt tta atg caa aat gtg ttt gca aat Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn 865 870 875 880	2640
tct ggt act att gct aat aaa cga gat agg gtc aac ttg caa ctt aat Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn 885 890 895	2688
ttg cta gaa tta ttt agc aat gca tta cag gga gtt gac tgg aag ttt Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe 900 905 910	2736
ctt att gat gtg gca ccg aaa att att cgt gac ttg aaa aat ttt aat Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn 915 920 925	2784
ggg ata ttt gac tcg ctt att cct ggt gtt caa ttg gac ttt gaa gtg Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val 930 935 940	2832
ttt gtc aaa ttg cat cat tca gtt gct gtg att aac tat cta ttt gaa Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu 945 950 955 960	2880
aac agg aca ttt tct gcc ttg ttt aag ctt gtt aat att gga gtt gat Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp 965 970 975	2928
tct gtg aat gaa tca ggt gaa tcg gcg gaa ttg gtg tca cat gcc ctt Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu 980 985 990	2976

ggg ttg att aat tct ttg ttg aga gtt caa aat tct ttt ata aac aag Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys 995 1000 1005	3024
ttg tta cca ata ttg cga aac aaa gat acg cag caa caa tta cat cgt Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg 1010 1015 1020	3072
ggg aca gcc att ggg att ggt act tct atg agt ctt gcg tta gca acc Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr 1025 1030 1035 1040	3120
cct aga acc ata ttt gat tgt ata tac tat cca aag aat ttg gga aca Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr 1045 1050 1055	3168
cat ggt gtt gct gat ttt tac gaa gtg ata ttg ttc cac tta tct gca His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala 1060 1065 1070	3216
gtt gtc caa ttt gcc ctt tat gtc agt tgt gaa aat act att tcc aac Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn 1075 1080 1085	3264
aaa gca att tcc ata ttg aaa gga gta agc caa tcc aag ttt ttt gtt Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val 1090 1095 1100	3312
acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu 1105 1110 1115 1120	3360
att acc aca ttt gaa aac atc gac gag tca ata aaa atc aag ttt gct Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala 1125 1130 1135	3408
ttc att gac aag ttt gaa gaa ctc gag gac tct ttg aat atg aaa tat Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr 1140 1145 1150	3456
gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys 1155 1160 1165	3504
gtg gct act act gcc cac ttt ttg ttg gga tac aaa gtg aaa ggc gat Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp 1170 1175 1180	3552
aca tta gac ttg gta cag aca aac gat caa aac aca tta cta aaa tct Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser 1185 1190 1195 1200	3600
ttc tta aat aca ttg agc att agt ctt gat ttg att tct gaa att gat Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp 1205 1210 1215	3648 -
tac aat aat ggt aat aac cat att att gat gtt ggt cca gcc aag ctt	3696

Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
1220 1225 1230	
tcg tcg ttg att tta cag att ctt atc aag ttg tgc caa gat cca att	3744
Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
1235 1240 1245	
tcg tcg tca ata aca ttg aat caa tta cgt gaa tat gaa gaa ttg ttt	3792
Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
1250 1255 1260	
gaa aaa ttg gtt aac tgt caa cct aaa ctt gat ttg aat acc gtt tgg	3840
Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp	
1265 1270 1275 1280	
tgt ggt aac cag ttt gat ggg gat ttg cag att gat gct agc aat gta	3888
Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
1285 1290 1295	
ttt gtt gac aac caa gca agc acc cag gct ttc ttt tcc ttt att aac	3936
Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	
1300 1305 1310	
cag aga aac tta att ttg cag tat ttg tca ttg gaa ttc cat agt gtc	3984
Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
1315 1320 1325	
aaa tca aga act aag cgg gag tat tat tct aaa gtg ttg acc aac gac	4032
Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
1330 1335 1340	
aag gaa ttt gtt aat cgt aca cct aag gtg ttg aca ttt tta aac att	4080
Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
1345 1350 1355 1360	
cta aat tat tca ttc aag aac ttt gaa gtg cag aaa tac gaa tgg ctt	4128
Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	
1365 1370 1375	
gac caa aaa ttt aac gtg tcg ttg tta ttg gca gaa gta aac gct caa	4176
Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln	
1380 1385 1390	
aag aat ggt aca tta gat ttt tct gtt tta aca aag gtt ttc cgt ctt	4224
Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu	
1395 1400 1405	
ttg tgc caa acg tca aac tta ata aca ccc gag tca aag caa ttg ttt	4272
Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe	
1410 1415 1420	
gcc gaa gaa att atg gtt gaa gga agt aag att tct gac ttt gtc aca	4320
Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr	
1425 1430 1435 1440	-
aag tac ctg gtg tcg acc gac ttg aag gat gtg cag ttg aaa tgc tta	4368
Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	

1445	1450	1455	
cat tca tgg tgt caa ttg ata gag att ttg gtt act gac agt gga atc His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile 1460 1465 1470			4416
aat tcg ctg aat ttc atc ttg gaa gtg ttg caa gtt att att ccc aaa Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys 1475 1480 1485			4464
atc aat gac tat ttt gat gtg gac ata ctg ttt tct gaa gaa atg gtt Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val 1490 1495 1500			4512
tca tta tgt gtt tta ttg ttt gat ctt tat gat cag ctg act ctt gcg Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala 1505 1510 1515 1520			4560
gac aga aaa ggt gaa gat ttt gca ctt gga att gag aga ttg atc ccc Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro 1525 1530 1535			4608
tta ttt cag act tgt att gca ggt att ctt aat tct aac tca aca ccc Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro 1540 1545 1550			4656
agc tta cgc tca gac ttg tat gta gtt ggc aac aag ttt ttg tta aaa Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys 1555 1560 1565			4704
tgt ttt gag aga gag tcg ttt ttg aaa caa gtg atg cat atc atc aag Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys 1570 1575 1580			4752
tcg gta gat aaa aag ttt ttc cag gtg att tgt aat gac gct atc tac Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr 1585 1590 1595 1600			4800
tca gag ggt cca tct aga atc act tct act tta ttc ctc gag tca tta Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu 1605 1610 1615			4848
gtt cac tta ggg act ttg gtc aag gtt gat ttt att ttg aat gcg ttg Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu 1620 1625 1630			4896
atc aaa aat aac gca ttg ctg ttg cta gtc agg tca gtt aag cgg act Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr 1635 1640 1645			4944
gat gcc atg atc aaa ttg tgc cag gaa aaa aat tca gga gtg act tta Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu 1650 1655 1660			4992
gat cat ttc ata ttt gac ttg atg gca ttc aaa gca acg cta tat ttt Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe 1665 1670 1675 1680			5040

ttt gtt aga gtg gcc aaa tcg aaa aac ggg gca ttg cag ttg att caa	5088
Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln	
1685 1690 1695	

aat gaa ttg ttt tca att ttg cat cag tcg aag ttt ttg cag att gat	5136
Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp	
1700 1705 1710	

cca gat att ggt tta agt tta cga att gaa gaa gtt caa gat cac aag	5184
Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys	
1715 1720 1725	

act gtc aat gta aat gtt ttg cta gat act cca ctt tcg ata act gac	5232
Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp	
1730 1735 1740	

ttg gtg gat cca tac aag ttg cga agt gaa aac act ata tca tat ttt	5280
Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe	
1745 1750 1755 1760	

gag ttc ctt gta cca ata ttt cag cta ctt aca aca gtg tta ttg tca	5328
Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser	
1765 1770 1775	

atg gga cca aat tat caa cct gca att att caa act aga gaa ctt atg	5376
Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met	
1780 1785 1790	

aag agt gta aat cga ttg gtg gta ggt gtt atg aaa aga gat ttc ttg	5424
Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu	
1795 1800 1805	

gta gag acc aaa caa att ggt caa ggg ttg tac aag gaa gag agt cac	5472
Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His	
1810 1815 1820	

gag ttg gta tcg ttg aaa gaa ttg gtg aag ttg ttt att ttg att gat	5520
Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp	
1825 1830 1835 1840	

tca tta gct cat tat agt gtg tag	5544
Ser Leu Ala His Tyr Ser Val	
1845	

<210> 11
 <211> 1847
 <212> PRT
 <213> Candida albicans

<400> 11	
Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr	
1 5 10 15	
Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe	
20 25 30	

Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 35 40 45
 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60
 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 65 70 75 80
 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 85 90 95
 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 100 105 110
 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 115 120 125
 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 130 135 140
 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
 145 150 155 160
 Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln
 165 170 175
 Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn
 180 185 190
 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
 195 200 205
 Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn
 210 215 220
 Ash Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu
 225 230 235 240
 Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys
 245 250 255
 Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys
 260 265 270
 Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser
 275 280 285
 Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu
 290 295 300
 Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
 305 310 315 320
 Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu
 325 330 335

Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu
 340 345 350
 Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp
 355 360 365
 Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro
 370 375 380
 Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu
 385 390 395 400
 Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile
 405 410 415
 Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro
 420 425 430
 Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val
 435 440 445
 Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu
 450 455 460
 Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu
 465 470 475 480
 Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu
 485 490 495
 Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe
 500 505 510
 Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly
 515 520 525
 Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu
 530 535 540
 Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu
 545 550 555 560
 Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu
 565 570 575
 Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe
 580 585 590
 Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile
 595 600 605
 Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met
 610 615 620
 Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys
 625 630 635 640

Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala
 645 650 655
 Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala
 660 665 670
 Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys
 675 680 685
 Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys
 690 695 700
 Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser
 705 710 715 720
 Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe
 725 730 735
 Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe
 740 745 750
 Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu
 755 760 765
 Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu
 770 775 780
 Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr
 785 790 795 800
 Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu
 805 810 815
 Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu
 820 825 830
 Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu
 835 840 845
 Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu
 850 855 860
 Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn
 865 870 875 880
 Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn
 885 890 895
 Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe
 900 905 910
 Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn
 915 920 925
 Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val
 930 935 940

Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu
945 950 955 960
Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp
965 970 975
Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu
980 985 990
Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys
995 1000 1005
Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg
1010 1015 1020
Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr
1025 1030 1035 1040
Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr
1045 1050 1055
His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala
1060 1065 1070
Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn
1075 1080 1085
Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val
1090 1095 1100
Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu
1105 1110 1115 1120
Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala
1125 1130 1135
Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr
1140 1145 1150
Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys
1155 1160 1165
Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp
1170 1175 1180
Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser
1185 1190 1195 1200
Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp
1205 1210 1215
Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu
1220 1225 1230
Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile
1235 1240 1245

Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe
 1250 1255 1260

Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp
 1265 1270 1275 1280

Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val
 1285 1290 1295

Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn
 1300 1305 1310

Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val
 1315 1320 1325

Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp
 1330 1335 1340

Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile
 1345 1350 1355 1360

Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu
 1365 1370 1375

Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln
 1380 1385 1390

Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu
 1395 1400 1405

Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
 1410 1415 1420

Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
 1425 1430 1435 1440

Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
 1445 1450 1455

His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
 1460 1465 1470

Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
 1475 1480 1485

Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
 1490 1495 1500

Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
 1505 1510 1515 1520

Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
 1525 1530 1535

Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
 1540 1545 1550

Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565
 Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580
 Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 585 1590 1595 1600
 Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
 1605 1610 1615
 Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
 1620 1625 1630
 Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
 1635 1640 1645
 Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
 1650 1655 1660
 Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
 665 1670 1675 1680
 Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
 1685 1690 1695
 Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
 1700 1705 1710
 Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
 1715 1720 1725
 Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
 1730 1735 1740
 Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
 745 1750 1755 1760
 Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
 1765 1770 1775
 Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
 1780 1785 1790
 Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1795 1800 1805
 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1810 1815 1820
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 825 1830 1835 1840
 Ser Leu Ala His Tyr Ser Val
 1845

<210> 12
<211> 575
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 12
gtttggtgac tcaacctacc accaatcgat ttacactctt cataagttct ctagtgttgaa 60
taattgcagg ttgataattt ggtccattg acaataacac tggtgtaagt agctgaaata 120
ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180
ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaaatat 360
atatntnttt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
aacacccaac ccnaaaaacac ccaacacctc catcttgtcc cgccttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaaac atacaccccc tcaacccctc ctccccaaca 540
aacctacctc cctcaactcc tatttcctcc ctccc 575

<210> 13
<211> 921
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(918)

<220>
<221> gene
<222> (1)..(918)
<223> gene CaOR110

<400> 13
atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat 48
Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
1 5 10 15
tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
20 25 30
ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala

35	40	45	
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct	192		
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala			
50 55 60			
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg	240		
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met			
65 70 75 80			
ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288		
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg			
85 90 95			
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336		
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg			
100 105 110			
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384		
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp			
115 120 125			
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432		
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile			
130 135 140			
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480		
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu			
145 150 155 160			
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528		
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala			
165 170 175			
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576		
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr			
180 185 190			
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624		
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser			
195 200 205			
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672		
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile			
210 215 220			
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720		
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly			
225 230 235 240			
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768		
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala			
245 250 255			
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816		
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala			
260 265 270			

ttg	aag	aaa	aat	gaa	caa	acc	aaa	tcc	gat	ggg	ccc	atc	act	gaa	tct	864
Leu	Lys	Lys	Asn	Glu	Gln	Thr	Lys	Ser	Asp	Gly	Pro	Ile	Thr	Glu	Ser	
		275					280					285				

aaa act tga 921
Lys Thr
305

<400> 14
Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
1 5 10 15

Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
35 40 45

Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
65 70 75 80

Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
100 105 110

Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
130 135 140

Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
165 170 175

Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
180 185 190

Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser

195	200	205
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile		
210	215	220
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly		
225	230	235 240
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala		
	245	250 255
Glu Asp Ile Ala Gln Arg Lys Ala Ala Glu Ala Glu Ala Lys Ala		
	260	265 270
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser		
	275	280 285
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg		
	290	295 300
Lys Thr		
305		

<210> 15
 <211> 1454
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Splice Variant

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> gene CaOR110 Splice Variant

<400> 15	
atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat	48
Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn	
1 5 10 15	
tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac	96
Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp	
20 25 30	
ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc	144
Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala	
35 40 45	
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct	192
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala	
50 55 60	
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg	240
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met	
65 70 75 80	

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg	
85 90 95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg	
100 105 110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp	
115 120 125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile	
130 135 140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe	
290 295 300	

tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa	960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu	
305 310 315 320	
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat	1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn	
325 330 335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat	1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp	
340 345 350	
cat cca tta gta aaa ata tct aac aat act ata tct gct caa ggc tcg	1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser	
355 360 365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act	1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr	
370 375 380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att	1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile	
385 390 395 400	
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat	1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp	
405 410 415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat	1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn	
420 425 430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt	1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu	
435 440 445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga	1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly	
450 455 460	
caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct	1440
Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala	
465 470 475 480	
aga gcc aaa ggt aa	1454
Arg Ala Lys Gly	

<210> 16

<211> 484

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Splice Variant

<400> 16

Met	Thr	Ile	Glu	Thr	Ile	Tyr	Ile	Ala	Arg	His	Gly	Tyr	Arg	Ser	Asn
1				5					10					15	

Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
 165 170 175
 Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
 180 185 190
 Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser
 195 200 205
 Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
 210 215 220
 Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe
 290 295 300
 Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu
 305 310 315 320

Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn
 325 330 335
 Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp
 340 345 350
 His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser
 355 360 365
 Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr
 370 375 380
 His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile
 385 390 395 400
 Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp
 405 410 415
 Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn
 420 425 430
 Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu
 435 440 445
 Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly
 450 455 460
 Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala
 465 470 475 480
 Arg Ala Lys Gly

<210> 17
 <211> 2877
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(2874)

<220>
 <221> gene
 <222> (1)..(2874)
 <223> gene CaMR212

<400> 17
 atg aat ttg ttt caa cat aaa cat caa aaa tta ata tta caa tgt tat 48
 Met Asn Leu Phe Gln His Lys His Gln Lys Leu Ile Leu Gln Cys Tyr
 1 5 10 15

cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt 96
 Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser
 20 25 30

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg	144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val	
35 40 45	
att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt	192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg	
50 55 60	
act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa	240
Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys	
65 70 75 80	
aaa tgt agt gaa aac ttg aat gtt ttt gcc ttt caa gtg tgc tat atc	288
Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile	
85 90 95	
ttg caa ctg att gcc aac act aag gat ctt gcc ttg tgt aaa aat gtt	336
Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val	
100 105 110	
gtc aaa aca ttt ggt gtt ttg tgt gaa aac ttg gat ggt ggg ttg ttc	384
Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe	
115 120 125	
aca ggt gat aag gag ttt ata aag att ttc act gaa gtt ttc caa aca	432
Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr	
130 135 140	
tta gtt tcc ttt ggt aag gac aga tcg ggt gtt act cag tat gat tgg	480
Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp	
145 150 155 160	
cag atg att tct tta atg gct ata aat gat ata tcc agt tgt ttg agt	528
Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser	
165 170 175	
tat aat gca gct gtt ggt aaa aag ttt att gct ttg tcg att cct gtt	576
Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val	
180 185 190	
tta ctt cag ttt att att gca aac aac cca caa agc agc ata ttg caa	624
Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln	
195 200 205	
aga ttg aaa tcg aat ctc cac gtt gaa gat gat ggg aag agg ttg tca	672
Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser	
210 215 220	
cgt gct cat ctg caa aaa tcc cat agc aaa att gcc caa caa att gat	720
Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp	
225 230 235 240	
gat gat ttc acc aat gat tct tta acc ttg aca gat atc act gaa aag	768
Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys	
245 250 255	
gca ttt tcg tcg atg aaa tct ttt ttc aat acc aat gct gcc agt caa	816

Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln	
260 265 270	
atc tct gaa gtg aca aga gct gtt gtc caa cac aat att ctc aat gga	864
Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly	
275 280 285	
acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
290 295 300	
att cca gtt caa tta cgt ttt gtc agt ttg tcc acc ttg ttg gcc act	960
Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
305 310 315 320	
tta ggt aga att aat att gaa ggt aac acc aaa tcc aat tac aac atg	1008
Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
325 330 335	
caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
340 345 350	
aac atg att ggg tta tca gtt tca gat att att caa cag ttg tta tcg	1104
Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
355 360 365	
ttg caa gct gat ttg att ttg aag gca agt gat ttg gac aaa agt gaa	1152
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	
att tca att tta aca gac att tat tct gac tgt att tgt agt ttg act	1200
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
385 390 395 400	
aca cat ata tat tac ttt gat caa gtc ccg gac tcg att caa gaa atc	1248
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
405 410 415	
tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
420 425 430	
aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
435 440 445	
ttg gat aac att tcg aag att ttt tta att ttg aag aat aaa tca agc	1392
Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser	
450 455 460	
tca att aat cgt aac cat gtg aat ttg gaa cat tgg gat atc agt tta	1440
Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu	
465 470 475 480	
gga tta ttg gct cca caa ggc gac cat gat gat aac aga aaa atg att	1488
Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile	